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EXAMINER	
SWITZER, JULIET CAROLINE	
ART UNIT	**PAPER NUMBER**
1634	

DATE MAILED: 03/30/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/613,765	AUSUBEL ET AL.	
	Examiner	Art Unit	
	Juliet C. Switzer	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *35 and 59-65* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *35 and 59-65* is/are rejected.

7)☒ Claim(s) *35* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *20 July 2003* is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *4/04*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Claims 35 and 59-65 are pending and examined herein.

2. Claim 35 is objected to because it refers to the nucleotide sequence "of Fig. 2." MPEP 2173(s) states "Where possible, claims are to be complete in themselves. Incorporation by reference to a specific figure or table "is permitted only in exceptional circumstances where there is no practical way to define the invention in words and where it is more concise to incorporate by reference than duplicating a drawing or table into the claim. Incorporation by reference is a necessity doctrine, not for applicant's convenience." In this case, applicant is advised to amend the claims to refer to SEQ ID NO instead of to the drawing.

Claim Rejections - 35 USC § 112

3. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

4. Claim 35 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 35 is indefinite over the recitation "isolating disease resistance gene or a portion thereof in plants having sequence identity to RPS2" because this recitation is confusing because it is not clear if "having sequence identity to RPS2" is meant to modify the plants or the disease resistance gene or a portion thereof. Furthermore it is not clear what it means to isolate a gene "in plants" because it is not clear if applicant is merely trying to set forth that the gene or portion is isolated from a plant, or if the isolating takes place in plants that have a gene that has identity to RPS2.

5. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Scope of Enablement

6. Claims 35 and 59-65 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for methods for isolating or identifying the presence of a plant resistance gene comprising the sequence of SEQ ID NO: 1 in a sample taken from *Arabadopsis thaliana,* isolating or identifying the presence of a plant resistance gene comprising the sequence of SEQ ID NO: 137 in a sample taken from tomato, or for isolating or detecting the presence of a plant resistance gene encoding the L6 polypeptide of flax in a flax sample (L6 sequence show in Figure 5 A and B), or for isolating or detecting the presence of a plant resistance gene encoding the N polypeptide of tobacco in a tobacco sample (N sequence show in Figure 5 A and B), does not reasonably provide enablement for methods for identifying or isolating any additional genes encoding plant resistance genes. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims.

The following factors have been considered in formulating this rejection (*In re Wands,* 858F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988): the breadth of the claims, the predictability or unpredictability of the art, the amount of direction or guidance presented, the presence or absence of working examples of the invention and the quantity of experimentation necessary.

Breadth of the Claims and Nature of the Invention

Claim 35 is drawn to a method of isolating a disease resistance gene or a portion of a disease resistance gene comprising steps of amplifying by PCR the disease resistance gene or portion thereof and isolating the gene or portion. The claim very broadly describes the primers as being at least 13 nucleotides in length and as having "regions of complementarity" to opposite strands of the nucleic acid sequence of Figure 2. The claims do not define the length of the requisite "regions of complementarity," and so effectively, the claims encompass the use of primers that have any minimal region of complementarity, including only a single nucleotide. So, due to the broad language used in the claims, there is effectively no structural limitation on the primers used in the claim. The nature of the invention, however, is very specific in that the claims set forth that by this amplification a disease resistance gene, or a portion of a disease resistance gene would be isolated. The nature of the invention requires that the claimed invention result in the isolation of a disease resistance gene, and thus implies that amplification with any primer pair that has any level of complementarity with RPS2 will result in the isolation of a disease resistance gene.

Claim 59 also recites isolating a disease resistance gene or a fragment thereof via amplification of plant cell DNA. In claim 59, the primers are described as "having homology to a conserved region of an RPS disease-resistance gene." Like in claim 35, however, the level of homology is entirely undefined, so this recitation is very broad. The "conserved region of an RPS disease-resistance gene" is not particularly defined in the specification, but the specification does set forth that a "conserved region" of the polypeptides is a stretch of at least six amino acids that has a minimum of 30% identity between a minimum of two of the disclosed RPS family members- Rps2, L6, N, or Prf (p. 14). Thus, this recitation is extremely broad as a "conserved

region" can be as few as 2 amino acids in common between only two of the four polypeptides. Thus, the primers used in claim 59 have to have some undefined level of sequence homology to any potential "conserved" two amino acid stretch between the polypeptides. Claims 60 and 61 further define the amplification methodology but not the sequences of the primers.

Claim 62 is a method for identifying a plant disease resistance gene via hybridization with a labeled DNA sequence- with the only limitation on the probe being that it has "homology to a conserved region of an RPS disease-resistance gene." Like in claim 59, this is an extremely broad recitation. Further, the breadth of this recitation is complicated by the fact that the claim sets forth that the hybridization conditions are sufficiently low so as only 50% identity is necessary for detection, yet the claim sets forth that plant disease resistance genes are identified by this hybridization event. Claim 63 recites that the probe is produced by the isolation method of claim 59, and claim 64 further describes the preparation being assayed. Claim 65 is very similar in scope to claim 63, except that it includes a further step of isolating the sequence.

For each of claims 35, 59-61 and 65, the nature of the invention, however, is very specific in that the claims set forth that by the recited amplification a disease resistance gene, or a portion of a disease resistance gene will be isolated. The nature of the invention requires that the claimed invention result in the isolation of a disease resistance gene, and thus implies that amplification with any primer pair meets the broadly stated requirements in the claims will result in the isolation of a disease resistance gene. Likewise for claim 62, the nature of the invention specifically sets forth that a disease resistance gene is detected by the hybridization event.

Guidance in the Specification and Working Examples

The specification defines a "disease resistance gene" as encoding a polypeptide capable of triggering a defense response in a plant cell or tissue (p. 10), and in particular an "RPS gene" as "disease resistance gene having about 50% or greater sequence identity to the RPS2 sequence of Fig. 2 or *a portion thereof* (p. 10, emphasis added)." On page 14, the specification defines an "RPS disease-resistance gene" as "any member of the family of plant genes characterized by their ability to trigger a plant defense response and having at least 20%, preferably 30%, and most preferably 50% amino acid sequence identity to one of the conserved regions of one RPS members described herein (p. 14)

The specification teaches the isolation and cloning of a plant resistance gene referred to as RPS2 and having instant SEQ ID NO: 1 (p. 29 and following). The specification teaches that the RPS2 polypeptide does not resemble the protein structure of the previously cloned plant resistance gene Pto (p. 32), and that RPS2 encodes a polypeptide that contains a number of structural motifs, including a P-loop and an LRR domain, but also a leucine zipper and a transmembrane spanning domain (specification, p. 32 and 39-40). The specification further teaches that these regions are also present in three additional disease resistance polypeptides, namely the N protein, the L6 protein and the Prf protein (p. 41), and further teaches that by using oligonucleotides for the detection of these domains, other members of the "RPS gene family" can be isolated (p. 41).

However, the specification provides no conclusive evidence that any and all additional genes which comprises the recited elements is in fact a plant resistance gene. The claims are very broadly drawn to encompass the detection and isolation of resistance genes based on very

limited commonalities with the disclosed genes. While the data in the specification support the assertion that there is a class of disease resistance genes that have common structural domains (P-loop and an LRR domain, but also a leucine zipper and a transmembrane spanning domain), this is not the same as teaching that every gene that is amplified by primers that have "regions of complementarity" to RPS2 (as recited in claim 35) or that encodes a polypeptide with any "conserved region" of an RPS gene is in fact a disease resistance gene. There is not a nexus between the observations of the specification and the particular assertions set forth regarding the ability to isolate "disease resistance genes." Due to the breadth of the claimed methods, the practice of the methods commensurate in scope with the claims could be expected to isolate hundreds of thousands of possible genes or fragments thereof, and it is highly unpredictable which ones of these would be "disease resistance genes."

The specification teaches an assay for screening candidate plant resistance genes to determine if they do in fact cause a disease-resistance response, and exemplify this method with instant SEQ ID NO: 1 and A. thaliana challenged with P. syringae (beginning at page 47). It is highly unpreidctable whether this system would be successful in identifying a plant resistance gene in a case where the potential pathogen is unknown in any possible plant species due to the very specific nature of the interaction between a resistance gene and pathogen. Furthermore, the instant methods recite isolating a plant resistance gene or a fragment of a plant resistance gene, with the fragment having no requisite length. The specification does not provide any guidance as to how to identify if a fragment is in fact part of a plant resistance gene. The specification does not provide any guidance as to what portion of SEQ ID NO: 1 or the other discussed plant

resistance genes are necessary for functioning of the protein to induce the hypersensitive response.

The specification does not provide any working examples in which any plant resistance are isolated or identified using the claimed invention. The specification is entirely prophetic with regard to the use of hybridization or amplification based methods to SEQ ID NO: 1 or to RPS conserved regions as a means for isolating (discovering) new resistance genes. While the method for detecting the sequences using fragments of SEQ ID NO: 1 or fragments of genes encoding the N, L6 or PFR polypeptides may be enabled, the additional use of the other genes or probes from within other genes is not provided by the instant specification, largely because the sequence of these genes is totally unpredictable based on the instant disclosure. Further, once such sequences are isolated or identified, there is no way to predict whether or not they are actually disease resistance genes.

State of the Prior Art and Level of Unpredictability

The prior art at the time the invention was filed does not teach any other plant resistance genes which comprise an LRR domain and a P-loop. The level of unpredictability with regard to the sequence and structure of other such genes is quite high, since ostensibly these genes would be derived from different plant species and would probably have different functions. Leucine rich repeats and P-loops are motifs that are present in a variety of proteins of diverse function. For example, LRRs are present in proteins involved in hormone-receptor interactions, enzyme inhibition, cell adhesion and cellular trafficking (InterPro record IPR001611, entitled Leucine-rich repeat). The P-loop motif is present in any protein that binds ATP or GTP, including proteins with a variety of functions such as ATP synthases, nitrogenase iron protein family, and

DNA mismatch repair proteins (PROSITE: PDOCOOO17, entitled ATP/GTP-binding site motif A (P-loop)). The specification has not established any correlative relationship between these ubiquitous structures and plant resistance, the specification has only shown that they are present in some plant resistance genes.

There are hundreds of thousands of possible plant resistance genes when one considers that there are a hundreds of plant pathogens and hundreds of plant species. The structure and mode of action of these putative plant resistance genes is entirely unpredictable. The disclosure of a single working example of a single gene encoding a polypeptide that has a single set of two motifs is not sufficient to establish a sufficient pattern to predict the structure of other plant resistance genes. A single data point is not conclusive to establish a pattern, as applicants have asserted. For example, the post filing date art of Lawrence *et al.* (Current Plant Science and Biotechnology in Agriculture (1994) 3: 303-6) discuss the rust-resistance gene from flax (encoding the so called L6 polypeptide), yet the sequence described by Lawrence *et al.* has no significant similarity to other sequences known at the time (p. 305). The specification does not provide any evidence to establish that the domains discussed in the specification are sufficient to be descriptive of an entire class of genes.

Further, the claims are so broadly drawn that the encompass the use of any possible probe or primer with very little structure specifically required by the claims. Encompassed within applicants claims are probes which comprise and primers which hybridize to any number of unknown sequences. There is no predictable method for identifying these primers or probes.

Quantity of Experimentation Necessary

A high degree of experimentation would be necessary to develop other probes and/or primers useful for the practice of the claimed invention. In order to establish that there is a correlative relationship between plant resistance genes and genes which would be isolated by the claimed methods, the practitioner would be required to sequence hundreds of plant genes, determine the presence of the domains in the genes, confirm that the genes are in fact plant resistance genes, and using this information show that the common features in the genes are correlative to plant resistance genes. Furthermore, a similar amount of work would be required to develop primers that would hybridize to any nucleic acid molecule containing the domains in question, if such primers were to exist. This volume of experimentation in itself would be considered inventive.

Even if a relationship has been established demonstrating that there is a "class" of plant resistance genes have any or all of the structures discussed in the specification, that does not necessarily mean that all nucleic acids which encode polypeptides comprising these structures are plant resistance genes, as the claims imply. The instant claims are drawn to methods for identifying or isolating other nucleic acids that encode plant resistance genes. According to the method, one would use a hybridization probe that would detect a gene that is a fragment of SEQ ID NO: 1 or which is part of a "conserved" RPS domain, and upon detection of hybridization, conclude that a plant resistance gene is present. Applicant has referred in the specification to four different plant resistance genes, but it does not appear any of them were discovered using any variation of the claimed methods. Instead, the plant resistance genes were isolated using processes in which it was known at the time of discovery which pathogen was inducing the plant

resistance response. This is a significant difference from the claims of the instant methods wherein the possible plant resistance genes would be isolated based on the structural characteristics of the encoded polypeptides without knowledge of the relevant pathogen to which resistance is imparted.

Plant resistance genes (and the encoded polypeptides) develop in nature in response to specific pathogens. That is, plant resistance is not a generalized response where any particular plant resistance gene confers resistance to a wide variety of pathogens. Instead, as is exemplified in the instant specification and in the post filing date art, plant resistance genes encode polypeptides that are each particular to specific pathogens. The gene disclosed in the instant specification encodes a polypeptide that confers resistance to a specific pathogen (a bacterial pathogen). Likewise in the L6 polypeptide and the N polypeptide confer resistance to particular pathogens (a fungal and a viral pathogen). Because plant resistance to pathogens is such a specific event, where specific plant proteins are successful at conferring resistance against specific pathogens, a screening assay which first identifies a putative plant resistance gene by general structural features is many steps away from actually identifying a plant resistance gene. The actual experimentation necessary to confirm that a putative gene identified by the claimed methods is in fact a plant resistance gene would require screening the putative gene in transgenic plants against hundreds of thousands or millions of possible plant pathogens considering all of the possible viral, fungal, and bacterial pathogens that attach plants. Given that the relationship between conferring plant resistance and pathogens is a highly specific relationship, it would be totally unpredictable to determine among all of the possible bacterial, fungal, and viral plant pathogens which pathogen a particular gene may confer resistance against. This is particularly

relevant because it would make it nearly impossible discern whether a negative result in a test of resistance would indicate that an isolated gene is not a plant resistance gene or if the practitioner were simple testing the wrong pathogen.

Furthermore, the instant claims are drawn to the use of any probe which would hybridize to any portion of a gene encoding a plant resistance gene or the use of any probe which as any degree of homology to a gene encoding any two amino acids in common between RPS polypeptides. Applicant has not provided the structure of any of these portions from other genes, nor has applicant provided additional flanking sequences from other genes which are encompassed within the probes and primers recited in the instant claims. Even if the claims were limited to the use of probes to particular domains, applicant has provided no evidence that these motifs are specific to plant resistance genes. That is, in order to confirm that a gene detected using the claimed methods is in fact a plant resistance gene, an extensive, and undue, amount of experimentation would be required to be undertaken by a practitioner. Such experimentation would require extensive experimentation to identify the function of the encoded polypeptide in a plant.

As noted above, the specification has provided no evidence that every gene which has these features is a plant resistance gene. Furthermore, with regard to the selection of probes and primers, the selection of probes and primers which may be useful in the claimed invention from within SEQ ID NO: 1 is enabled by the specification. The selection of other probes and primers from sequences totally undisclosed or described is not provided by the instant specification. To this end, a the law is clear that a patent application must be read in light of the specification and not in a vacuum. In this case, as discussed in the rejection, the specification provides only for

the selection of primers and probes from within a very particular sequences that are disclosed in the specification, but the claims are broadly drawn to include the use of any of a multiplicity of different primers and probes.

It is further reiterated that even if the selection of primers and probes that are specific to particular domains were routine, the claims are drawn to methods for isolating and identifying the presence of plant resistance genes in a sample, and the claims depend on the unsubstantiated assertion by applicant that any gene detected by the hybridization and amplification events set forth in the claims is a plant resistance gene. Furthermore, as previously noted, while the claims require a probe or primer that "has homology" to particular sequences named in the claims, the probes and primers are not limited to binding only these domains, and encompass the use of probes and primers to other portions of undisclosed and undiscovered resistance genes.

Conclusion

Because of the high level of unpredictability concerning the sequence of other probes useful for practicing this invention, the lack of guidance as to how to construct such probes, the lack of such teaching in the prior art, and the high quantity of experimentation necessary to identify such probes, the present specification does not contain enabling disclosure for the ordinary practitioner to practice this invention in its broad scope. Due to these factors the examiner concludes that undue experimentation would be necessary to practice the presently claimed invention.

Written Description

7. Claims 1-19 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The current claims are drawn to a method which detects any of the genus of any plant resistance genes which have regions of complementarity to instant SEQ ID NO: 1 or to "conserved regions" of RPS resistance genes. The full scope of the claims is discussed in the enablement rejection. The claims require the use of a primer or probe that hybridizes to such a gene. These probes encompass many molecules which bind with some portion of the recited regions but also which may bind with any other portion of the putative resistance genes, including undiscovered full length molecules that encode resistance genes. This large genus is represented in the specification by a limited number of sequences, namely SEQ ID NO: 1 and SEQ ID NO: 137. In addition, genes encoding the recited amino acid sequence of the L6 polypeptide and the N polypeptide are described. Thus applicant has express possession of only a limited number of species in a genus which comprises hundreds of millions of different possibilities.

The court has made it clear that with regard to chemical compounds, the standard for written description is possession, not enablement or intent to claim. "While we have no doubt a person so motivated would be enabled by the specification to make it, this is beside the point for the question is not whether he would be so enabled but whether the specification discloses the compound to him, specifically, as something appellants actually invented. We think it does not."

In Re Ruschig, 379 F.2d 990, 995, 154 U.S.P.Q. 118, 123 (CCPA 1967). Furthermore, the court stated "Accordingly, naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." The Regents of the University of California v. Eli Lilly & Co., 43 U.S.P.Q.2d 1406 (Federal Circuit 1997). In the instant case, although applicnats have provided a general function (plant resistance gene) and a general structure (having a P-loop and LRR domain) for the probes used in the claimed methods, and for the resistance genes that are the target of hybridization and amplification, these even taken together are not sufficient to convey possession of the entire possible group of plant resistance genes whose use as full length probes or whose use as portions (i.e. primers or shorter probes) are encompassed by the instant claims. The fact that these genes have some degree of homology to disclosed sequences is not sufficient to provide the specific sequences which are essential for their use as probes or for the use of any hybridizing portion of these genes as primers and probes.

Specifically, the possession test requires that the inventor, at the time of invention, is able to identify what was claimed. In a situation such as this, where the only structural information provided is that the resultant protein have one of the twenty amino acids, leucine, present at some unidentified level, combined with a P loop, is insufficient to demonstrate possession. P loops are found in a variety of different proteins, such as nucleotide and nucleoside kinases, chloramphenicol phosphotransferase, adenosine-5'phosphosulfate kinase, PAPS sulfotransferase, G proteins, RNA helicase and motor proteins. Therefore, the presence of this element is not, in combination with the presence of leucine, sufficient to distinguish one class of proteins from

another. Thus, it is not clear that Applicant has possession of the genus of probes required to practice the claimed methods.

Because these method claims are dependent upon specific probes for detection, possession of probes which may or may not fall within the regions claimed is particularly important. Since the "conserved regions" comprise a small fraction of the protein sequence, the entire remaining sequence, not disclosed by applicant nor specifically delineated in the specification, falls within the scope of these claims. This remaining sequence, which has no functional or structural limitation in the specification, can be used for probe design within the scope of the claimed methods. However, there is no possession of these sequences.

With regard to the written description, all of these claims require the use of nucleic acid sequences different from those disclosed in the specification for which no written description is provided in the specification.

It is noted that in Fiers v. Sugano (25 USPQ2d, 1601), the Fed. Cir. concluded that

> "...if inventor is unable to envision detailed chemical structure of DNA sequence coding for specific protein, as well as method of obtaining it, then conception is not achieved until reduction to practice has occurred, that is, until after gene has been isolated...conception of any chemical substance, requires definition of that substance other than by its functional utility."

In the instant application, only the SEQ ID NO: 1 and SEQ ID NO: 137 and nucleic acids encoding the disclosed amino acid sequence of the N and L6 genes are described, and therefore, methods which utilize fragments of these sequences are also considered described. Also, in Vas-Cath Inc. v. Mahurkar (19 USPQ2d 1111, CAFC 1991), it was concluded that:

> "...Appellant must also convey, with reasonable clarity to those skilled in art, that Appellant, as of filing date sought, was in possession of invention, with invention being, for purposes of "written description" inquiry, whatever is presently claimed."

The broad claims encompass the use of a genus of nucleic acids that were not described at the time of the invention. In the application at the time of filing, there is no record or description which would demonstrate conception or written description of any plant resistance gene which has amino acids modified by addition, insertion, deletion, substitution or inversion from the disclosed plant resistance genes and polypeptides but retaining correlative function for use in the claimed methods.

Double Patenting

8. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

9. Claims 35, 59-65 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-19 of copending Application No. 09/608288. Although the conflicting claims are not identical, they are not patentably distinct from each other. The claims of the conflicting application teach methods for detecting plant resistance genes via amplification and hybridization using probes which bind to P-loop and LRR domains in a sample, specifically setting forth that the probe or primers hybridize to SEQ ID NO: 1 or sequence having at least 50% identity to SEQ ID NO: 1, and that the sample is and extract of plant material. The claims differ from the instantly claimed because they do not recite a step of isolating the detected plant resistance gene. However, it would have been prima facie obvious to one of ordinary skill in the art to have isolated the plant resistance genes detected by the methods set forth in the conflicting application for the purpose of further analysis and study of the detected genes.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Conclusion

10. No claim is allowed.

11. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Juliet C Switzer whose telephone number is (571) 272-0753. The

examiner can normally be reached on Monday, Tuesday, or Thursday, from 9:00 AM until 4:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached by calling (571) 272-0735.

The fax phone numbers for the organization where this application or proceeding is assigned are (571) 273-8300. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571)272-0507.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-

9199.

Juliet C. Switzer
Primary Examiner
Art Unit 1634

March 20, 2006